Version With Markings to Show Changes

Accession No.	Description	Smith-Waterman Score	% Identity
Z36531	Homo sapiens fibrinogen-like protein	500	38.462

A polypeptide was predicted to be encoded by SEQ ID NO: 2 as set forth below. The polypeptide was predicted using a software program called FASTY (available from http://fasta.bioch.virginia.edu) which selects a polypeptide based on a comparison of translated novel polynucleotide to known polypeptides (W.R. Pearson, Methods in Enzymology, 183: 63-98 (1990), herein incorporated by reference).

Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid segment	Predicted end nucleotide location corresponding to last amino acid residue of amino acid segment	AMINO ACID SEGMENT (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
3	717	[DLKDTIGSVTKTPSGLYIIHPEGSSYPFEVMCDMDY RGGGWTVIQKRIDGIIDFQRLWCDYLDGFGDLLGEF WLGLKKIFYIVNQKNTSFMLYVALESEDDTLAYASY DNFWLEDETRFFKMHLGRYSGNAGDAFRGLKKED NQNAMPFSTSDVDNDGCRPACLVNGQSVKSCSHLH NKTGWWFNECGLANLNGIHHFSGKLLATGIQWGT WTKNNSPVKIKSVSMKIRRMYNPYKF]Asp Leu Lys Asp Thr Ile Gly Ser Val Thr Lys Thr Pro Ser Gly Tyr Ile Ile His Pro Glu Ser Ser Tyr Pro Phe Glu Val Met Cys Asp Met AspTyr Arg Gly Gly Gly Trp Thr Val Ile Gln Lys Arg Ile Asp Gly Ile Ile Asp Phe Gln Arg Leu Trp Cys Asp Tyr Leu Asp Gly Phe Gly Asp Leu Leu Gly Glu Phe Trp Leu Gly Leu Lys Lys Ile Phe Tyr Ile Val Asn Gln Lys Asn Thr Ser Phe Met Leu Tyr Al Ala Leu Glu Ser Glu Asp Asp Thr Leu Ala Tyr Ala Ser Tyr Asp Asn Phe Trp Leu Glu Asp Glu Thr Arg Phe Phe Lys Met His Leu Gly Arg Tyr Ser Gly Asn Ala Gly Asp Ala Phe Arg Gly Leu Lys Lys Glu

		Asp Asn Gln Asn Ala Met Pro Phe Ser Thr Ser Asp Val Asp Asn Asp Gly Cys Arg Pro Ala Cys Leu Val Asn Gly Gln Ser Val Lys Ser Cys Ser His Leu His Asn Lys Thr Gly Trp Trp Phe Asn Glu Cys Gly Leu Ala Asn Leu Asn Gly Ile His His Phe Ser Gly Lys Leu Leu Ala Thr Gly Ile Ghn Trp Gly Thr Trp Thr Lys Asn Asn Ser Pro Val Lys Ile Lys Ser Val Ser Met Lys Ile Arg Arg Met Tyr Asn Pro Tyr Lys Phe

EXAMPLE 3

ASSEMBLAGE OF SEQ ID NO: 3

Assembly of novel nucleotide sequence of SEQ ID NO: 3 was accomplished by using an EST sequence SEQ ID NO: 1 as a seed. The seed was extended by using software programs such as BLAST and Hyseq proprietary software to pull additional sequences from Hyseq's proprietary database containing EST sequences and by gel sequencing (377 Applied Biosystems (ABI) sequencer) using primers to extend the 3' end. Inclusion of component sequences into the assemblage was based BLAST scores greater than 1000 and a p-value of p-3 (depending on the length of homology). The 5' end was extended using RACE, as disclosed in Marathon-Ready™ cDNA User Manual (PT1156-1) (Clontech), herein incorporated by reference.

EXAMPLE 4

A. Expression of SEQ ID NO: 4 - 9 in cells

Chinese Hamster Ovary (CHO) cells or other suitable cell types are grown in DMEM (ATCC) and 10% fetal bovine serum (FBS) (Gibco) to 70% confluence. Prior to transfection the media is changed to DMEM and 0.5% FCS. Cells are transfected with cDNAs for SEQ ID NO: 3 with pBGal vector by the FuGENE-6 transfection reagent (Boehringer). In summary, 4 µl of FuGENE-6 is diluted in 100 µl of DMEM and incubated for 5 minutes. Then, this is added to 1 µg of DNA and incubated for 15 minutes before adding it to a 35 mm dish of CHO cells. The CHO cells are incubated at 37°C with 5% CO_2. After 24 hours, media and cell lysates are collected, centrifuged and dialyzed against assay buffer (15 mM Tris pH 7.6, 134 mM NaCl, 5 mM glucose, 3 mM $CaCl_2$ and $MgCl_2$.

B. Expression Study Using SEQ ID NO: 3

The expression of SEQ ID NO: 3 in various tissues is analyzed using a semi-quantitative polymerase chain reaction-based technique. Human cDNA libraries are used as sources of expressed genes from tissues of interest (adult bladder, adult brain, adult heart, adult kidney, adult lymph node, adult liver, adult lung, adult ovary, adult placenta, adult rectum, adult spleen, adult testis, bone marrow, thymus, thyroid gland, fetal kidney, fetal liver, fetal liver-spleen, fetal skin, fetal brain, fetal leukocyte and macrophage). Gene-specific primers are used to amplify portions of the SEQ ID NO: 3 sequence from the samples. Amplified products are separated on an agarose gel, transferred and chemically linked to a nylon filter. The filter is then hybridized with a radioactively labeled (^{33}P-dCTP) double-stranded probe generated from SEQ ID NO: 3 using a Klenow polymerase, random-prime method. The filters are washed (high stringency) and used to expose a phosphorimaging screen for several hours. Bands indicate the presence of cDNA including SEQ ID NO: 3 sequences in a specific library, and thus mRNA expression in the corresponding cell type or tissue.